SEQUENCE LISTING

<110> Kulp, David C.
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Williams, Alan J.
Harmon, Cyrus L.

<120> Nucleic Acids Encoding G Proteins Coupled Receptors

<130> 3379.1

<140> 10/038,895
<141> 2001-10-24

<150> US 60/244,082
<151> 2000-10-26

<160> 20

<170> PatentIn version 3.2

<210> 1
<211> 274
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (126)..(126)
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<220>
<221> misc_feature
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<223> Xaa can be any naturally occurring amino acid

<400> 1

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Leu Leu Ala Pro Thr Gly Ser Leu Phe Arg Asn Cys Thr Gln Asp Gly
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Trp Ser Glu Thr Phe Pro Arg Pro Asn Leu Ala Cys Gly Val Asn Val
            20                  25                  30

Asn Asp Ser Ser Asn Glu Lys Arg Ser Tyr Leu Leu Lys Leu Lys Val
        35                  40                  45

Met Tyr Thr Val Gly Tyr Ser Ser Ser Leu Val Met Leu Leu Val Ala
    50                  55                  60

Leu Gly Ile Leu Cys Ala Phe Arg Arg Leu His Cys Thr Arg Asn Tyr
65                  70                  75                  80

Ile His Met His Leu Phe Val Ser Phe Ile Leu Arg Ala Leu Ser Asn
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85 90 95

Phe Ile Lys Asp Ala Val Leu Phe Ser Ser Asp Asp Val Thr Tyr Cys
100 105 110

Asp Ala His Arg Gly Cys Lys Leu Val Met Val Leu Phe Xaa Tyr Cys
115 120 125

Ile Met Ala Asn Tyr Ser Trp Leu Leu Val Glu Gly Ser Thr Phe Thr
130 135 140

His Xaa Leu Ala Ile Ser Phe Phe Ser Glu Arg Lys Tyr Leu Gln Gly
145 150 155 160

Phe Val Ala Phe Gly Trp Gly Ser Pro Ala Ile Phe Val Ala Leu Trp
165 170 175

Ala Ile Ala Arg His Phe Leu Glu Asp Val Gly Cys Trp Asp Ile Asn
180 185 190

Ala Asn Ala Ser Ile Trp Trp Ile Ile Arg Gly Pro Val Ile Leu Ser
195 200 205

Ile Leu Asn Phe Ile Leu Phe Ile Asn Ile Leu Arg Ile Leu Met Arg
210 215 220

Lys Leu Arg Thr Gln Glu Thr Arg Gly Asn Glu Val Ser His Tyr Lys
225 230 235 240

Arg Leu Ala Arg Ser Thr Leu Leu Leu Ile Pro Leu Phe Gly Ile His
245 250 255

Tyr Ile Val Phe Ala Phe Ser Pro Glu Asp Ala Met Glu Ile Gln Leu
260 265 270

Phe Phe

<210> 2
<211> 381
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 2
ctcttggcac ccacaggttc cttgttccga aactgcacac aggatggctg gtcagaaacc 60

ttccccaggc ctaatctggc ctgtggcgtt aatgtgaacg actcttccaa cgagaagcgg 120

cactcctacc tgctgaagct gaaagtcatg tacaccgtgg gctacagctc ctccctggtc 180

atgctcctgg tcgcccttgg catcctctgt gctttccgga ggctccactg cactcgcaac 240

tacatccaca tgcacctgtt cgtgtccttc atccttcgtg ccctgtccaa cttcatcaag 300

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aagctggtca tggtgctgtt c 381

<210> 3
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<212> DNA
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<220>
<223> Synthetic Organism

<220>
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<222> (58)..(58)
<223> n is a, c, g, or t

<400> 3
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ctcgccatct ccttcttctc tgaaagaaag tacctccagg gatttgtggc attcggatgg 120

ggttctccag ccatttttgt tgctttgtgg gctattgcca gacactttct ggaagatgtt 180

gggtgctggg acatcaatgc caacgcatcc atctggtgga tcattcgtgg tcctgtgatc 240

ctctccatcc tgattaattt catccttttc ataaacattc taagaatcct gatgagaaaa 300

cttagaaccc aagaaacaag aggaaatgaa gtcagccatt ataagcgcct ggccaggtcc 360

actctcctgc tgatcccccc ctttggcatc cactacatcg tcttcgcctt ctccccagag 420

gacgctatgg agatccagct gtttttt 447

<210> 4
<211> 828
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<220>
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<222> (439)..(439)
<223> n is a, c, g, or t

<400> 4
ctcttggcac ccacaggttc cttgttccga aactgcacac aggatggctg gtcagaaacc 60

ttccccaggc ctaatctggc ctgtggcgtt aatgtgaacg actcttccaa cgagaagcgg 120

cactcctacc tgctgaagct gaaagtcatg tacaccgtgg gctacagctc ctccctggtc 180

atgctcctgg tcgcccttgg catcctctgt gctttccgga ggctccactg cactcgcaac 240

tacatccaca tgcacctgtt cgtgtccttc atccttcgtg ccctgtccaa cttcatcaag 300

gacgccgtgc tcttctcctc agatgatgtc acctactgcg atgcccacag ggcgggctgc 360

aagctggtca tggtgctgtt ctactgcatc atggccaact actcctggct gctggtggaa 420

ggctctacct tcacacatnt cctcgccatc tccttcttct ctgaaagaaa gtacctccag 480

ggatttgtgg cattcggatg gggttctcca gccatttttg ttgctttgtg ggctattgcc 540

agacactttc tggaagatgt tgggtgctgg gacatcaatg ccaacgcatc catctggtgg 600

atcattcgtg gtcctgtgat cctctccatc ctgattaatt tcatcctttt cataaacatt 660

ctaagaatcc tgatgagaaa acttagaacc caagaaacaa gaggaaatga agtcagccat 720

tataagcgcc tggccaggtc cactctcctg ctgatccccc tctttggcat ccactacatc 780

gtcttcgcct tctccccaga ggacgctatg gagatccagc tgtttttt 828

<210> 5
<211> 320
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 5

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Pro Thr Phe Ile Leu Phe Ser Phe Gln Pro Gly Asp Lys Arg Thr Lys
1               5                   10                  15

His Ile Cys Val Tyr Trp Glu Gly Ser Glu Gly Gly His Trp Ser Thr
            20                  25                  30

Glu Gly Cys Ser His Val His Ser Asn Gly Ser Tyr Thr Lys Cys Lys
        35                  40                  45

Cys Phe His Leu Ser Ser Phe Ala Val Leu Val Ala Leu Ala Pro Lys
    50                  55                  60

Asp Pro Val Leu Thr Val Ile Thr Gln Val Gly Leu Thr Ile Ser Leu
65                  70                  75                  80

Leu Cys Leu Phe Leu Ala Ile Leu Thr Phe Leu Leu Cys Arg Pro Ile
                85                  90                  95

Gln Asn Thr Ser Thr Ser Leu His Leu Glu Leu Ser Leu Cys Leu Phe
            100                 105                 110
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Leu Ala His Leu Leu Phe Leu Thr Gly Ile Asn Arg Thr Glu Pro Glu
        115                 120                 125

Leu Cys Ser Ile Ile Ala Gly Leu Leu His Phe Leu Tyr Leu Ala Cys
    130                 135                 140

Phe Thr Trp Met Leu Leu Glu Gly Leu His Leu Phe Leu Thr Val Arg
145                 150                 155                 160

Asn Leu Lys Val Ala Asn Tyr Thr Ser Thr Gly Arg Phe Lys Lys Arg
                165                 170                 175

Phe Met Tyr Pro Val Gly Tyr Gly Ile Pro Ala Val Ile Ile Ala Val
            180                 185                 190

Ser Ala Ile Val Gly Pro Gln Asn Tyr Gly Thr Phe Thr His Cys Trp
        195                 200                 205

Leu Lys Leu Asp Lys Gly Phe Ile Trp Ser Phe Met Gly Pro Val Ala
    210                 215                 220

Val Ile Ile Leu Asn Leu Val Phe Tyr Phe Gln Val Leu Trp Ile Leu
225                 230                 235                 240

Arg Ser Lys Leu Ser Ser Leu Asn Lys Glu Val Ser Thr Ile Gln Asp
                245                 250                 255

Thr Arg Val Met Thr Phe Lys Ala Ile Ser Gln Leu Phe Ile Leu Gly
            260                 265                 270

Cys Ser Trp Gly Leu Gly Phe Phe Met Val Glu Glu Val Gly Lys Thr
        275                 280                 285

Ile Gly Ser Ile Ile Ala Tyr Ser Phe Thr Ile Ile Asn Thr Leu Gln
    290                 295                 300

Gly Val Leu Leu Phe Val Val His Cys Leu Leu Asn Arg Gln Val Arg
305                 310                 315                 320
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<210> 6
<211> 969
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Organism

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aacggttctt acaccaaatg caagtgcttc catctgtcca gctttgccgt cctcgtggct 180

cttgccccca aggaggaccc tgtgctgacc gtgatcaccc aggtggggct gaccatctct 240

ctgctgtgcc tcttcctggc catcctcacc ttcctcctgt gccggcccat ccagaacacc 300

agcacctccc tccatctaga gctctccctc tgcctcttcc tggcccacct cctgttcctg 360

acgggcatca acagaactga gcctgaggtg ctgtgctcca tcattgcagg gctgctgcac 420

ttcctctacc tggcttgctt cacctggatg ctcctggaag ggctgcacct cttcctcacc 480

gtcaggaacc tcaaggtggc caactacacc agcacgggca gattcaagaa gaggttcatg 540

taccctgtag gctacgggat cccagctgtg attattgctg tgtcagcaat agttggaccc 600

cagaattatg gaacatttac tcactgttgg ctcaagcttg ataaaggatt catctggagc 660

ttcatggggc cagtagcagt cattatcttg ataaacctgg tgttctactt ccaagttctg 720

tggattttga gaagcaaact ttcctccctc aataaagaag tttccaccat tcaggacacc 780

agagtcatga catttaaagc catttctcag ctatttatcc tgggctgttc ttggggcctt 840

ggtttttta tggttgaaga agtagggaag acgattggat caatcattgc atactcattc 900

accatcatca acacccttca gggagtgttg ctctttgtgg tacactgtct ccttaatcgc 960

caggtaagg 969

<210> 7
<211> 217
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 7

Gln His Ser Asp Ala Val His Asp Leu Leu Leu Asp Val Ile Thr Trp
1 5 10 15

Val Gly Ile Leu Leu Ser Leu Val Cys Leu Leu Ile Cys Ile Phe Thr
20 25 30

Phe Cys Phe Phe Arg Gly Leu Gln Ser Asp Arg Asn Thr Ile His Lys
35 40 45

Asn Leu Cys Ile Ser Leu Phe Val Ala Glu Leu Leu Phe Leu Ile Gly
50 55 60

Ile Asn Arg Thr Asp Gln Pro Ala Cys Ala Val Phe Ala Ala Leu Leu
65 70 75 80

```
His Phe Phe Phe Leu Ala Ala Phe Thr Trp Met Phe Leu Glu Gly Val
                85                  90                  95

Gln Leu Tyr Ile Met Leu Val Glu Val Phe Glu Ser Glu His Ser Arg
            100                 105                 110

Arg Lys Tyr Phe Tyr Leu Val Gly Tyr Gly Met Pro Ala Leu Ile Val
        115                 120                 125

Ala Val Ser Ala Ala Val Asp Tyr Arg Ser Tyr Gly Thr Asp Lys Val
    130                 135                 140

Cys Trp Leu Arg Leu Asp Thr Tyr Phe Ile Trp Ser Phe Ile Gly Pro
145                 150                 155                 160

Ala Thr Leu Ile Ile Met Asn Val Ile Phe Leu Gly Ile Ala Leu Tyr
                165                 170                 175

Lys Met Phe His His Thr Ala Ile Leu Lys Pro Glu Ser Gly Cys Leu
            180                 185                 190

Asp Asn Ile Lys Leu Lys Ile Asn Ile Pro Ile Ile Lys Ser Ile Tyr
        195                 200                 205

Ile Tyr Met Tyr Ile Cys Met Cys Val
    210                 215
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<210> 8
<211> 657
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 8

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ctgtcccttg tttgtctcct gatttgcatc ttcacatttt gctttttccg ggggctccag    120

agtgaccgta acaccatcca caagaacctc tgcatcagtc tctttgtagc agagctgctc    180

ttcctgattg ggatcaaccg aactgaccaa ccaattgcct gtgctgtttt cgctgccctg    240

ttacatttct tcttcttggc tgccttcacc tggatgttcc tggaggggtt gcagctttat    300

atcatgctgg tggaggtttt tgagagtgaa cattcacgta ggaaatactt ttatctggtc    360

ggctatggga tgcctgcact cattgtggct gtgtcagctg cagtagacta caggagttat    420

ggaacagata aagtatgttg gctccgactt gacacctact tcatttggag ttttatagga    480

ccagcaactt tgataattat gcttaatgta atcttccttg ggattgcttt atataaaatg    540
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tttcatcata ctgctatact gaaacctgaa tcaggctgtc ttgataacat caagttaaaa 600

attaatattc caattataaa atctatttat atctatatgt atatatgcat gtgtgtg 657

<210> 9
<211> 304
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 9

Gly Asn Val Ala Val Ala Phe Val Tyr Tyr Lys Ser Ile Gly Pro Leu
1 5 10 15

Leu Ser Ser Ser Asp Asn Phe Leu Leu Lys Pro Gln Asn Tyr Asp Asn
20 25 30

Ser Glu Glu Glu Glu Arg Val Ile Ser Ser Val Ile Ser Val Ser Met
35 40 45

Ser Ser Asn Pro Pro Thr Leu Tyr Glu Leu Glu Lys Ile Thr Phe Thr
50 55 60

Leu Ser His Arg Lys Thr Asp Arg Tyr Arg Ser Leu Cys Ala Phe Trp
65 70 75 80

Asn Tyr Ser Pro Asp Thr Met Asn Gly Ser Trp Ser Ser Glu Gly Cys
85 90 95

Glu Leu Thr Tyr Ser Asn Glu Thr His Thr Ser Cys Arg Cys Asn His
100 105 110

Leu Thr His Phe Ala Ile Leu Met Ser Ser Gly Pro Ser Ile Ile Lys
115 120 125

Asp Tyr Asn Ile Leu Thr Arg Ile Thr Gln Leu Gly Ile Ile Ile Ser
130 135 140

Leu Ile Cys Leu Ala Ile Cys Ile Phe Thr Phe Trp Phe Phe Ser Glu
145 150 155 160

Ile Gln Ser Thr Arg Thr Thr Ile His Lys Asn Leu Cys Cys Ser Leu
165 170 175

Phe Leu Ala Glu Leu Val Phe Leu Val Gly Ile Asn Thr Asn Thr Asn
180 185 190

Lys Phe Cys Ser Ile Ile Ala Gly Leu Leu His Tyr Phe Phe Leu Ala
195 200 205

Ala Phe Ala Trp Met Cys Ile Glu Gly Ile His Leu Tyr Leu Ile Val
210 215 220

Val Gly Val Ile Tyr Asn Lys Gly Phe Leu His Lys Asn Phe Tyr Ile
225 230 235 240

Phe Gly Tyr Leu Ser Pro Ala Val Val Val Gly Phe Ser Ala Ala Leu
245 250 255

Gly Tyr Arg Tyr Tyr Gly Thr Thr Lys Val Cys Trp Leu Ser Thr Glu
260 265 270

Asn Asn Phe Ile Trp Ser Phe Ile Gly Pro Ala Cys Leu Ile Ile Leu
275 280 285

Val Cys Ile Tyr Lys Ile Val Ile Thr Ile Gln Lys Ser Asp Asp His
290 295 300

<210> 10
<211> 921
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Organism

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gacaacttct tattgaaacc tcaaaattat gataattctg aagaggagga aagagtcata 120

tcttcagtaa tttcagtctc aatgagctca aacccaccca cattatatga acttgaaaaa 180

ataacattta cattaagtca tcgaaaggtc acagataggt ataggagtct atgtgcattt 240

tggaattact cacctgatac catgaatggc agctggtctt cagagggctg tgagctgaca 300

tactcaaatg agacccacac ctcatgccgc tgtaatcacc tgacacattt tgcaattttg 360

atgtcctctg gtccttccat tggtattaaa gattataata ttcttacaag gatcactcaa 420

ctaggaataa ttatttcact gatttgtctt gccatatgca tttttacctt ctggttcttc 480

agtgaaattc aaagcaccag gacaacaatt cacaaaaatc tttgctgtag cctatttctt 540

gctgaacttg tttttcttgt tgggatcaat acaaatacta ataagctctt ctgttcaatc 600

attgccggac tgctacacta cttcttttta gctgcttttg catggatgtg cattgaaggc 660

atacatctct atctcattgt tgtgggtgtc atctacaaca agggattttt gcacaagaat 720

ttttatatct ttggctatct aagcccagcc gtggtagttg gattttcggc agcactagga 780

tacagatatt atggcacaac caaagtatgt tggcttagca ccgaaaacaa ctttatttgg 840

agttttatag gaccagcatg cctaatcatt cttgtatgta tatataaaat tgttattaca 900

attcaaaaaa gtgatgatca t 921

<210> 11
<211> 203
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 11

Gly Ala Trp Ala Thr Thr Gly Cys Ser Val Ala Ala Leu Tyr Leu Asp
1 5 10 15

Ser Thr Ala Cys Phe Cys Asn His Ser Thr Ser Phe Ala Ile Leu Leu
20 25 30

Gln Ile Tyr Glu Val Gln Gly Pro Glu Glu Glu Ser Leu Leu Arg Thr
35 40 45

Leu Ser Phe Val Gly Cys Gly Val Ser Phe Cys Ala Leu Thr Thr Thr
50 55 60

Phe Leu Leu Phe Leu Val Ala Gly Val Pro Lys Ser Glu Arg Thr Thr
65 70 75 80

Val His Lys Asn Leu Thr Phe Ser Leu Ala Ser Ala Glu Gly Phe Leu
85 90 95

Met Thr Ser Glu Trp Ala Lys Ala Asn Glu Ala Cys Val Ala Val Thr
100 105 110

Val Ala Met His Phe Leu Phe Leu Val Ala Phe Ser Trp Met Leu Val
115 120 125

Glu Gly Leu Leu Leu Trp Arg Lys Val Val Ala Val Ser Met His Pro
130 135 140

Gly Pro Gly Met Arg Leu Tyr His Ala Thr Gly Trp Gly Val Pro Val
145 150 155 160

Gly Ile Val Ala Val Thr Leu Ala Met Leu Pro His Asp Tyr Val Ala
165 170 175

Pro Gly His Cys Trp Leu Asn Val His Thr Asn Ala Ile Trp Ala Phe
180 185 190

Val Gly Pro Val Leu Phe Val Leu Thr Val Ser
195 200

<210> 12
<211> 615
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 12
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ttctgcaacc acagcaccag ctttgccatc ctgctgcaaa tctatgaagt acagagaggc 120

cctgaggagg agtcgctgct gaggactctg tcatttgtgg gctgtggcgt gtccttctgc 180

gccctcacca ccaccttctt gctcttcctg gtggccgggg tccccaagtc agagcgaacc 240

acagtccaca agaacctcac cttctccctg gcctctgccg agggcttcct catgaccagc 300

gagtgggcca aggccaatga ggtggcatgt gtggctgtca cagtcgcaat gcacttcctc 360

tttctggtgg cattctcctg gatgctggtg gaggggctgc tgctgtggag gaaggtggta 420

gctgtgagca tgcacccggg cccaggcatg cggctctacc acgccacagg ctggggcgtg 480

cctgtgggca tcgtggcggt caccctggcc atgctccccc atgactacgt ggcccccgga 540

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gtgctgactg tgagc 615

<210> 13
<211> 1339
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 13

Met Lys Ser Pro Arg Arg Thr Thr Leu Cys Leu Met Phe Ile Val Ile
1 5 10 15

Tyr Ser Ser Lys Ala Ala Leu Asn Trp Asn Tyr Glu Ser Thr Ile His
20 25 30

Pro Leu Leu His Glu His Glu Pro Ala Gly Glu Glu Ala Leu Arg Gln
35 40 45

Lys Arg Ala Val Ala Thr Lys Ser Pro Thr Ala Glu Glu Tyr Thr Val
50 55 60

```
Asn Ile Glu Ile Ser Phe Glu Asn Ala Ser Phe Leu Asp Pro Ile Lys
65                  70                  75                  80

Ala Tyr Leu Asn Ser Leu Ser Phe Pro Ile His Gly Asn Asn Thr Asp
                85                  90                  95

Gln Ile Thr Asp Ile Leu Ser Ile Asn Val Thr Thr Val Cys Arg Pro
            100                 105                 110

Ala Gly Asn Glu Ile Trp Cys Ser Cys Glu Thr Gly Tyr Gly Trp Pro
        115                 120                 125

Arg Glu Arg Cys Leu His Asn Leu Ile Cys Gln Glu Arg Asp Val Phe
    130                 135                 140

Leu Pro Gly His His Cys Ser Cys Leu Lys Glu Leu Pro Pro Asn Gly
145                 150                 155                 160

Pro Phe Cys Leu Leu Gln Glu Asp Val Thr Leu Asn Met Arg Val Arg
                165                 170                 175

Leu Asn Val Gly Phe Gln Glu Asp Leu Met Asn Thr Ser Ser Ala Leu
            180                 185                 190

Tyr Arg Ser Tyr Lys Thr Asp Leu Glu Thr Ala Arg Lys Gly Tyr Gly
        195                 200                 205

Ile Leu Pro Gly Phe Lys Gly Val Thr Val Thr Gly Phe Lys Ser Gly
    210                 215                 220

Ser Val Val Val Thr Tyr Glu Val Lys Thr Thr Pro Pro Ser Leu Glu
225                 230                 235                 240

Leu Ile His Lys Ala Asn Glu Gln Val Val Gln Ser Leu Asn Gln Thr
                245                 250                 255

Tyr Lys Met Asp Tyr Asn Ser Phe Gln Ala Val Thr Ile Asn Glu Ser
            260                 265                 270

Asn Phe Phe Val Thr Pro Glu Ile Ile Phe Glu Gly Asp Thr Val Ser
        275                 280                 285

Leu Val Cys Glu Lys Glu Val Leu Ser Ser Asn Val Ser Trp Arg Tyr
    290                 295                 300

Glu Glu Gln Gln Leu Glu Ile Gln Asn Ser Ser Arg Phe Ser Ile Tyr
305                 310                 315                 320
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Thr Ala Leu Phe Asn Asn Met Thr Ser Val Ser Lys Leu Thr Ile His
                325                 330                 335

Asn Ile Thr Pro Gly Asp Ala Gly Glu Tyr Val Cys Lys Leu Ile Leu
            340                 345                 350

Asp Ile Phe Glu Tyr Glu Cys Lys Lys Lys Ile Asp Val Met Pro Ile
        355                 360                 365

Gln Ile Leu Ala Asn Glu Glu Met Lys Val Met Cys Asp Asn Asn Pro
    370                 375                 380

Val Ser Leu Asn Cys Cys Ser Gln Gly Asn Val Asn Trp Ser Lys Val
385                 390                 395                 400

Glu Trp Lys Gln Glu Gly Lys Ile Asn Ile Pro Gly Thr Pro Glu Thr
                405                 410                 415

Asp Ile Asp Ser Ser Cys Ser Arg Tyr Thr Leu Lys Ala Asp Gly Thr
            420                 425                 430

Gln Cys Pro Ser Gly Ser Ser Gly Thr Thr Val Ile Tyr Thr Cys Glu
        435                 440                 445

Phe Ile Ser Ala Tyr Gly Ala Arg Gly Ser Ala Asn Ile Lys Val Thr
    450                 455                 460

Phe Ile Ser Val Ala Asn Leu Thr Ile Thr Pro Asp Pro Ile Ser Val
465                 470                 475                 480

Ser Glu Gly Gln Asn Phe Ser Ile Lys Cys Ile Ser Asp Val Ser Asn
                485                 490                 495

Tyr Asp Glu Val Tyr Trp Asn Thr Ser Ala Gly Ile Lys Ile Tyr Gln
            500                 505                 510

Arg Phe Tyr Thr Thr Arg Arg Tyr Leu Asp Gly Ala Glu Ser Val Leu
        515                 520                 525

Thr Val Lys Thr Ser Thr Arg Glu Trp Asn Gly Thr Tyr His Cys Ile
    530                 535                 540

Phe Arg Tyr Lys Asn Ser Tyr Ser Ile Ala Thr Lys Asp Val Ile Val
545                 550                 555                 560

His Pro Leu Pro Leu Lys Leu Asn Ile Met Val Asp Pro Leu Glu Ala
```

565 570 575

Thr Val Ser Cys Ser Gly Ser His His Ile Lys Cys Cys Ile Glu Glu
580 585 590

Asp Gly Asp Tyr Lys Val Thr Phe His Thr Gly Ser Ser Ser Leu Pro
595 600 605

Ala Ala Lys Glu Val Asn Lys Lys Gln Val Cys Tyr Lys His Asn Phe
610 615 620

Asn Ala Ser Ser Val Ser Trp Cys Ser Lys Thr Val Asp Val Cys Cys
625 630 635 640

His Phe Thr Asn Ala Ala Asn Asn Ser Val Trp Ser Pro Ser Met Lys
645 650 655

Leu Asn Leu Val Pro Gly Glu Asn Ile Thr Cys Gln Asp Pro Val Ile
660 665 670

Gly Val Gly Glu Pro Gly Lys Val Ile Gln Lys Leu Cys Arg Phe Ser
675 680 685

Asn Val Pro Ser Ser Pro Glu Ser Pro Ile Gly Gly Thr Ile Thr Tyr
690 695 700

Lys Cys Val Gly Ser Gln Trp Glu Glu Lys Arg Asn Asp Cys Ile Ser
705 710 715 720

Ala Pro Ile Asn Ser Leu Leu Gln Met Ala Lys Leu Ile Lys Ser Pro
725 730 735

Ser Gln Asp Glu Met Leu Pro Thr Tyr Leu Lys Asp Leu Ser Ile Ser
740 745 750

Ile Asp Lys Ala Glu His Glu Ile Ser Ser Ser Pro Gly Ser Leu Gly
755 760 765

Ala Ile Ile Asn Ile Leu Asp Leu Leu Ser Thr Val Pro Thr Gln Val
770 775 780

Asn Ser Glu Met Met Thr Val Leu Ser Thr Val Asn Val Ile Leu Gly
785 790 795 800

Lys Pro Val Leu Asn Thr Trp Lys Val Leu Gln Gln Gln Trp Thr Asn
805 810 815

```
Gln Ser Ser Gln Leu Leu His Ser Val Glu Arg Phe Ser Gln Ala Leu
            820                 825                 830

Gln Ser Gly Asp Ser Pro Pro Leu Ser Phe Ser Gln Thr Asn Val Gln
        835                 840                 845

Met Ser Ser Met Val Ile Lys Ser Ser His Pro Glu Thr Tyr Gln Gln
    850                 855                 860

Arg Phe Val Phe Pro Tyr Phe Asp Leu Trp Gly Asn Val Val Ile Asp
865                 870                 875                 880

Lys Ser Tyr Leu Glu Asn Leu Gln Ser Asp Ser Ser Ile Val Thr Met
                885                 890                 895

Ala Phe Pro Thr Leu Gln Ala Ile Leu Ala Gln Asp Ile Gln Glu Asn
            900                 905                 910

Asn Phe Ala Glu Ser Leu Val Met Thr Thr Thr Val Ser His Asn Thr
        915                 920                 925

Thr Met Pro Phe Arg Ile Ser Met Thr Phe Lys Asn Asn Ser Pro Ser
    930                 935                 940

Gly Gly Glu Thr Lys Cys Val Phe Trp Asn Phe Arg Leu Ala Asn Asn
945                 950                 955                 960

Thr Gly Gly Trp Asp Ser Ser Gly Cys Tyr Val Glu Glu Gly Asp Gly
                965                 970                 975

Asp Asn Val Thr Cys Ile Cys Asp His Leu Thr Ser Phe Ser Ile Leu
            980                 985                 990

Met Ser Pro Asp Ser Pro Asp Pro  Ser Ser Leu Leu Gly  Ile Leu Leu
        995                 1000                1005

Asp Ile  Ile Ser Tyr Val Gly  Val Gly Phe Ser Ile  Leu Ser Leu
    1010                1015                1020

Ala Ala  Cys Leu Val Val Glu  Ala Val Val Trp Lys  Ser Val Thr
    1025                1030                1035

Lys Asn  Arg Thr Ser Tyr Met  Arg His Thr Cys Ile  Val Asn Ile
    1040                1045                1050

Ala Ala  Ser Leu Leu Val Ala  Asn Thr Trp Phe Ile  Val Val Ala
    1055                1060                1065
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Ala Ile Gln Asp Asn Arg Tyr Ile Leu Cys Lys Thr Ala Cys Val
1070 1075 1080

Ala Ala Thr Phe Phe Ile His Phe Phe Tyr Leu Ser Val Phe Phe
1085 1090 1095

Trp Met Leu Thr Leu Gly Leu Met Leu Phe Tyr Arg Leu Val Phe
1100 1105 1110

Ile Leu His Glu Thr Ser Arg Ser Thr Gln Lys Ala Ile Ala Phe
1115 1120 1125

Cys Leu Gly Tyr Gly Cys Pro Leu Ala Ile Ser Val Ile Thr Leu
1130 1135 1140

Gly Ala Thr Gln Pro Arg Glu Val Tyr Thr Arg Lys Asn Val Cys
1145 1150 1155

Trp Leu Asn Trp Glu Asp Thr Lys Ala Leu Leu Ala Phe Ala Ile
1160 1165 1170

Pro Ala Leu Ile Ile Val Val Val Asn Ile Thr Ile Thr Ile Val
1175 1180 1185

Val Ile Thr Lys Ile Leu Arg Pro Ser Ile Gly Asp Lys Pro Cys
1190 1195 1200

Lys Gln Glu Lys Ser Ser Leu Phe Gln Ile Ser Lys Ser Ile Gly
1205 1210 1215

Val Leu Thr Pro Leu Leu Gly Leu Thr Trp Gly Phe Gly Leu Thr
1220 1225 1230

Thr Val Phe Pro Gly Thr Asn Leu Val Phe His Ile Ile Phe Ala
1235 1240 1245

Ile Leu Asn Val Phe Gln Leu Phe Ile Leu Leu Phe Gly Cys Leu
1250 1255 1260

Trp Asp Leu Lys Gln Glu Ala Leu Leu Asn Lys Phe Ser Leu Ser
1265 1270 1275

Arg Trp Ser Ser Gln His Ser Lys Thr Ser Leu Gly Ser Ser Thr
1280 1285 1290

Pro Val Phe Ser Met Ser Ser Pro Ile Ser Arg Arg Phe Asn Asn
1295 1300 1305

Leu Phe Gly Lys Thr Gly Thr Tyr Asn Val Ser Thr Pro Glu Ala
1310 1315 1320

Thr Ser Ser Ser Leu Glu Asn Ser Ser Ser Ala Ser Ser Leu Leu
1325 1330 1335

Asn

<210> 14
<211> 4038
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Organism

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ccagctggtg aagaggcact gaggcaaaaa cgagccgttg ccacaaaaag tcctacggct 180

gaagaataca ctgttaatat tgagatcagt tttgaaaatg catccttcct ggatcctatc 240

aaagcctact tgaacagcct cagttttcca attcatggga ataacactga ccaaattacc 300

gacattttga gcataaatgt gacaacagtc tgcagacctg ctggaaatga aatctggtgc 360

tcctgcgaga caggttatgg gtggcctcgg gaaaggtgtc ttcacaatct catttgtcaa 420

gagcgtgacg tcttcctccc agggcaccat tgcagttgcc ttaaagaact gcctcccaat 480

ggacctttt gcctgcttca ggaagatgtt accctgaaca tgagagtcag actaaatgta 540

ggctttcaag aagacctcat gaacacttcc tccgccctct ataggtccta caagaccgac 600

ttggaaacag cgttccggaa gggttacgga attttaccag gcttcaaggg cgtgactgtg 660

acagggttca agtctggaag tgtggttgtg acatatgaag tcaagactac accaccatca 720

cttgagttaa tacataaagc caatgaacaa gttgtacaga gcctcaatca gacctacaaa 780

atggactaca actcctttca agcagttact atcaatgaaa gcaatttctt tgtcacacca 840

gaaatcatct ttgaagggga cacagtcagt ctggtgtgtg aaaaggaagt tttgtcctcc 900

aatgtgtctt ggcgctatga agaacagcag ttggaaatcc agaacagcag cagattctcg 960

atttacaccg cacttttcaa caacatgact tcggtgtcca agctcaccat ccacaacatc 1020

actccaggtg atgcaggtga atatgtttgc aaactgatat tagacatttt tgaatatgag 1080

tgcaagaaga aaatagatgt tatgcccatc caaattttgg caaatgaaga aatgaaggtg 1140

atgtgcgaca acaatcctgt atctttgaac tgctgcagtc agggtaatgt taattggagc 1200

aaagtagaat ggaagcagga aggaaaaata aatattccag gaacccctga gacagacata 1260

gattctagct gcagcagata caccctcaag gctgatggaa cccagtgccc aagcgggtcg 1320

tctggaacaa cagtcatcta cacttgtgag ttcatcagtg cctatggagc cagaggcagt 1380

gcaaacataa aagtgacatt catctctgtg gccaatctaa caataacccc ggacccaatt 1440

tctgtttctg agggacaaaa cttttctata aaatgcatca gtgatgtgag taactatgat 1500

gaggtttatt ggaacacttc tgctggaatt aaaatatacc aaagatttta taccacgagg 1560

aggtatcttg atggagcaga atcagtactg acagtcaaga cctcgaccag ggagtggaat 1620

ggaacctatc actgcatatt tagatataag aattcataca gtattgcaac caaagacgtc 1680

attgttcacc cgctgcctct aaagctgaac atcatggttg atcctttgga agctactgtt 1740

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tgctacaaac acaatttcaa tgcaagctca gtttcctggt gttcaaaaac tgttgatgtg 1920

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ctggttcctg gggaaaacat cacatgccag gatcccgtaa taggtgtcgg agagccgggg 2040

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atctctgccc caataaacag tctgctccag atggctaagg ctttgatcaa gagcccctct 2220

caggatgaga tgctccctac atacctgaag gatctttcta ttagcataga caaagcggaa 2280

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cagagttcac agctactaca ttcagtggaa agattttccc aagcattaca gtcgggagat 2520

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acttttaaga acaatagccc ttcaggcggc gaaacgaagt gtgtcttctg gaacttcagg 2880

cttgccaaca acacaggggg gtgggacagc agtgggtgct atgtagaaga aggtgatggg 2940

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ggcttttcca tcttgagctt ggcagcctgt ctagttgtgg aagctgtggt gtggaaatcg 3120

gtgaccaaga accggacttc ttatatgcgc cacacctgca tagtgaatat cgctgcctcc 3180

cttctggtcg ccaacacctg gttcattgtg gtcgctgcca tccaggacaa tcgctacata 3240

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ttcttctgga tgctgacact gggcctcatg ctgttctatc gcctggtttt cattctgcat 3360

gaaacaagca ggtccactca gaaagccatt gccttctgtc ttggctatgg ctgcccactt 3420

gccatctcgg tcatcacgct gggagccacc cagccccggg aagtctatac gaggaagaat 3480

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tccattggag acaagccatg caagcaggag aagagcagcc tgtttcagat cagcaagagc 3660

attggggtcc tcacaccact cttgggcctc acttggggtt ttggtctcac cactgtgttc 3720

ccagggacca accttgtgtt ccatatcata tttgccatcc tcaatgtctt ccagggatta 3780

ttcattttac tctttggatg cctctgggat ctgaaggtac aggaagcttt gctgaataag 3840

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cctgtgtttt ctatgagttc tccaatatca aggagattta acaatttgtt tggtaaaaca 3960

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gcttcttcgt tgctcaac 4038

<210> 15
<211> 460
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 15

Ile Leu Asn Ser Lys Ser Ile Ser Asn Trp Thr Phe Ile Arg Asp Arg
1 5 10 15

Asn Ser Ser Tyr Ile Leu Leu His Ser Val Asn Ser Phe Ala Arg Arg
20 25 30

Leu Phe Ile Asp Asn Ile Pro Val Asp Ile Ser Asp Val Phe Ile His
35 40 45

Thr Met Gly Thr Thr Ile Ser Gly Asp Asn Ile Gly Lys Asn Phe Thr
50 55 60

Phe Ser Met Arg Ile Asn Asp Thr Ser Asn Glu Val Thr Gly Arg Val
65 70 75 80

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Leu Ile Ser Arg Asp Glu Leu Arg Lys Val Pro Ser Pro Ser Gln Val
                85                  90                  95

Ile Ser Ile Ala Phe Pro Thr Ile Gly Ala Ile Leu Glu Ala Ser Leu
            100                 105                 110

Leu Glu Asn Val Thr Val Asn Gly Leu Val Leu Ser Ala Ile Leu Pro
        115                 120                 125

Lys Glu Leu Lys Arg Ile Ser Leu Ile Phe Glu Lys Ile Ser Lys Ser
    130                 135                 140

Glu Glu Arg Arg Thr Gln Cys Val Gly Trp His Ser Val Glu Asn Arg
145                 150                 155                 160

Trp Asp Gln Gln Ala Cys Lys Met Ile Gln Glu Asn Ser Gln Gln Ala
                165                 170                 175

Val Cys Lys Cys Arg Pro Ser Lys Leu Phe Thr Ser Phe Ser Ile Leu
            180                 185                 190

Met Ser Pro His Ile Leu Glu Ser Leu Ile Leu Thr Tyr Ile Thr Tyr
        195                 200                 205

Val Gly Leu Gly Ile Ser Ile Cys Ser Leu Ile Leu Cys Leu Ser Ile
    210                 215                 220

Glu Val Leu Val Trp Ser Gln Val Thr Lys Thr Glu Ile Thr Tyr Leu
225                 230                 235                 240

Arg His Val Cys Ile Val Asn Ile Ala Ala Thr Leu Leu Met Ala Asp
                245                 250                 255

Val Trp Phe Ile Val Ala Ser Phe Leu Ser Gly Pro Ile Thr His His
            260                 265                 270

Lys Gly Cys Val Ala Ala Thr Phe Phe Val His Phe Phe Tyr Leu Ser
        275                 280                 285

Val Phe Phe Trp Met Leu Ala Lys Ala Leu Leu Ile Leu Tyr Gly Ile
    290                 295                 300

Met Ile Val Phe His Thr Leu Pro Lys Ser Val Leu Val Ala Ser Leu
305                 310                 315                 320

Phe Ser Val Gly Tyr Gly Cys Pro Leu Ala Ile Ala Ala Ile Thr Val
                325                 330                 335
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Ala Ala Thr Glu Pro Gly Lys Gly Tyr Leu Arg Pro Glu Ile Cys Trp
340 345 350

Leu Asn Trp Asp Met Thr Lys Ala Leu Leu Ala Phe Val Ile Pro Ala
355 360 365

Leu Ala Ile Val Val Val Asn Leu Ile Thr Val Thr Leu Val Ile Val
370 375 380

Lys Thr Gln Arg Ala Ala Ile Gly Asn Ser Met Phe Gln Glu Val Arg
385 390 395 400

Ala Ile Val Arg Ile Ser Lys Asn Ile Ala Ile Leu Thr Pro Leu Leu
405 410 415

Gly Leu Thr Trp Gly Phe Gly Val Ala Thr Val Ile Asp Asp Arg Ser
420 425 430

Leu Ala Phe His Ile Ile Phe Ser Leu Leu Asn Ala Phe Gln Phe Phe
435 440 445

Ile Leu Val Phe Gly Thr Ile Leu Asp Pro Lys Val
450 455 460

<210> 16
<211> 1383
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 16
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gacatatcag atgtcttcat tcatactatg ggcaccacca tatctggaga taacattgga 180

aaaaatttca ctttttctat gagaattaat gacaccagca atgaagtcac tgggagagtg 240

ttgatcagca gagatgaact tcggaaggtg ccttcccctt ctcaggtcat cagcattgca 300

tttccaacta ttggggctat tttggaagcc agtcttttgg aaaatgttac tgtaaatggg 360

cttgtcctgt ctgccatttt gcccaaggaa cttaaaagaa tctcactgat ttttgaaaag 420

atcagcaagt cagaggagag gaggacacag tgtgttggct ggcactctgt ggagaacaga 480

tgggaccagc aggcctgcaa aatgattcaa gaaaactccc agcaagctgt ttgcaaatgt 540

aggccaagca aattgtttac ctctttctca attcttatgt cacctcacat cttagagagt 600

ctgattctga cttacatcac atatgtaggc ctgggcattt ctatttgcag cctgatcctt 660

tgcttgtcca ttgaggtcct agtctggagc caagtgacaa agacagagat cacctattta 720

cgccatgtgt gcattgttaa cattgcagcc actttgctga tggcagatgt gtggttcatt 780

gtggcttcct ttcttagtgg cccaataaca caccacaagg gatgtgtggc agccacattt 840

tttgttcatt tcttttacct ttctgtattt ttctggatgc ttgccaaggc actccttatc 900

ctctatggaa tcatgattgt tttccatacc ttgcccaagt cagtcctggt ggcatctctg 960

ttttcagtgg gctatggatg ccctttggcc attgctgcca tcactgttgc tgccactgaa 1020

cctggcaaag gctatctacg acctgagatc tgctggctca actgggacat gaccaaagcc 1080

ctcctggcct tcgtgatccc agctttggcc atcgtggtag taaacctgat cacagtcaca 1140

ctggtgattg tcaagaccca gcgagctgcc attggcaatt ccatgttcca ggaagtgaga 1200

gccattgtga gaatcagcaa gaacatcgcc atcctcacac cacttctggg actgacctgg 1260

ggatttggag tagccactgt catcgatgac agatccctgg ccttccacat tatcttctcc 1320

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gta 1383

<210> 17
<211> 299
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 17

Gly Thr Thr Gly Asp Trp Ser Ser Glu Gly Cys Ser Thr Glu Val Arg
1 5 10 15

Pro Glu Gly Thr Val Cys Cys Cys Asp His Leu Thr Phe Phe Ala Leu
20 25 30

Leu Leu Pro Thr Leu Asp Gln Ser Thr Val His Ile Leu Thr Arg Ile
35 40 45

Ser Gln Ala Gly Cys Gly Val Ser Met Ile Phe Leu Ala Phe Thr Ile
50 55 60

Ile Leu Tyr Ala Phe Leu Arg Leu Ser Arg Glu Arg Phe Lys Ser Glu
65 70 75 80

Asp Ala Pro Lys Ile His Val Ala Leu Gly Gly Ser Leu Phe Leu Leu
85 90 95

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Asn Leu Ala Phe Leu Val Asn Val Gly Ser Gly Ser Lys Gly Ser Asp
            100                 105                 110

Ala Ala Cys Trp Ala Arg Gly Ala Val Phe His Tyr Phe Leu Leu Cys
        115                 120                 125

Ala Phe Thr Trp Met Gly Leu Glu Ala Phe His Leu Tyr Leu Leu Ala
    130                 135                 140

Val Arg Val Phe Asn Thr Tyr Phe Gly His Tyr Phe Leu Lys Leu Ser
145                 150                 155                 160

Leu Val Gly Trp Gly Leu Pro Ala Leu Met Val Ile Gly Thr Gly Ser
                165                 170                 175

Ala Asn Ser Tyr Gly Leu Tyr Thr Ile Arg Asp Arg Glu Asn Arg Thr
            180                 185                 190

Ser Leu Glu Leu Cys Trp Phe Arg Glu Gly Thr Thr Met Tyr Ala Leu
        195                 200                 205

Tyr Ile Thr Val His Gly Tyr Phe Leu Ile Thr Phe Leu Phe Gly Met
    210                 215                 220

Val Val Leu Ala Leu Val Val Trp Lys Ile Phe Thr Leu Ser Arg Ala
225                 230                 235                 240

Thr Ala Val Lys Glu Arg Gly Lys Asn Arg Lys Lys Val Leu Thr Leu
                245                 250                 255

Leu Gly Leu Ser Ser Leu Val Gly Val Thr Trp Gly Leu Ala Ile Phe
            260                 265                 270

Thr Pro Leu Gly Leu Ser Thr Val Tyr Ile Phe Ala Leu Phe Asn Ser
        275                 280                 285

Leu Gln Val Asp Phe Tyr Ile Leu Ile Phe Tyr
    290                 295
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<210> 18
<211> 900
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 18
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gtgtgctgct gtgaccacct gacctttttc gccctgctcc tgagacccac cttggaccag 120

tccacggtgc atatcctcac acgcatctcc caggcgggct gtggggtctc catgatcttc 180

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gaagatgccc caaagatcca cgtggccctg ggtggcagcc tgttcctcct gaatctggcc 300

ttcttggtca atgtggggag tggctcaaag gggtctgatg ctgcctgctg ggcccggggg 360

gctgtcttcc actacttcct gctctgtgcc ttcacctgga tgggccttga agccttccac 420

ctctacctgc tcgctgtcag ggtcttcaac acctacttcg ggcactactt cctgaagctg 480

agcctggtgg gctggggcct gcccgccctg atggtcatcg gcactgggag tgccaacagc 540

tacggcctct acaccatccg tgatagggag aaccgcacct ctctggagct atgctggttc 600

cgtgaaggga caaccatgta cgccctctat atcaccgtcc acggctactt cctcatcacc 660

ttcctctttg gcatggtggt cctggccctg gtggtctgga agatcttcac cctgtcccgt 720

gctacagcgg tcaaggagcg ggggaagaac cggaagaagg tgctcaccct gctgggcctc 780

tcgagcctgg tgggtgtgac atgggggttg gccatcttca ccccgttggg cctctccacc 840

gtctacatct ttgcactttt caactccttg caagttgatt tttacatatt gatcttctat 900

<210> 19
<211> 468
<212> PRT
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<220>
<221> misc_feature
<222> (370)..(370)
<223> Xaa can be any naturally occurring amino acid

<400> 19

Asn His Ile Leu Asp Thr Ala Ala Ile Ser Asn Trp Ala Phe Ile Pro
1 5 10 15

Asn Lys Asn Ala Ser Ser Asp Leu Leu Gln Ser Val Asn Leu Phe Ala
20 25 30

Arg Gln Leu His Ile His Asn Asn Ser Glu Asn Ile Val Asn Glu Leu
35 40 45

Phe Ile Gln Thr Lys Gly Phe His Ile Asn His Asn Thr Ser Glu Lys
50 55 60

Ser Leu Asn Phe Ser Met Ser Met Asn Asn Thr Thr Glu Asp Ile Leu
65 70 75 80

```
Gly Met Val Gln Ile Pro Arg Gln Glu Leu Arg Lys Leu Trp Pro Asn
                85                  90                  95

Ala Ser Gln Ala Ile Ser Ile Ala Phe Pro Thr Leu Gly Ala Ile Leu
            100                 105                 110

Arg Glu Ala His Leu Gln Asn Val Ser Leu Pro Arg Gln Val Asn Gly
        115                 120                 125

Leu Val Leu Ser Val Val Leu Pro Glu Arg Leu Gln Glu Ile Ile Leu
    130                 135                 140

Thr Phe Glu Lys Ile Asn Lys Thr Arg Asn Ala Arg Ala Gln Cys Val
145                 150                 155                 160

Gly Trp His Ser Lys Lys Arg Arg Trp Asp Glu Lys Ala Cys Gln Met
                165                 170                 175

Met Leu Asp Ile Arg Asn Glu Val Lys Cys Arg Cys Asn Tyr Thr Ser
            180                 185                 190

Val Val Met Ser Phe Ser Ile Leu Met Ser Ser Lys Ser Met Thr Asp
        195                 200                 205

Lys Val Leu Asp Tyr Ile Thr Cys Ile Gly Leu Ser Val Ser Ile Leu
    210                 215                 220

Ser Leu Val Leu Cys Leu Ile Ile Glu Ala Thr Val Trp Ser Arg Val
225                 230                 235                 240

Val Val Thr Glu Ile Ser Tyr Met Arg His Val Cys Ile Val Asn Ile
                245                 250                 255

Ala Val Ser Leu Leu Thr Ala Asn Val Trp Phe Ile Ile Gly Ser His
            260                 265                 270

Phe Asn Ile Lys Ala Gln Asp Tyr Asn Met Cys Val Ala Val Thr Phe
        275                 280                 285

Phe Ser His Phe Phe Tyr Leu Ser Leu Phe Phe Trp Met Leu Phe Lys
    290                 295                 300

Ala Leu Leu Ile Ile Tyr Gly Ile Leu Val Ile Phe Arg Arg Met Met
305                 310                 315                 320

Lys Ser Arg Met Met Val Ile Gly Phe Ala Ile Gly Tyr Gly Cys Pro
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325 330 335

Leu Ile Ile Ala Val Thr Thr Val Ala Ile Thr Glu Pro Glu Lys Gly
340 345 350

Tyr Ile Arg Pro Glu Ala Cys Trp Leu Asn Trp Asp Asn Thr Lys Ala
355 360 365

Leu Xaa Ala Phe Ala Ile Pro Ala Phe Val Ile Val Ala Val Asn Leu
370 375 380

Ile Val Val Leu Val Val Ala Val Asn Thr Gln Arg Pro Ser Ile Gly
385 390 395 400

Ser Ser Lys Ser Gln Asp Val Val Ile Ile Met Arg Ile Ser Lys Asn
405 410 415

Val Ala Ile Leu Thr Pro Leu Leu Gly Leu Thr Trp Gly Phe Gly Ile
420 425 430

Ala Thr Leu Ile Glu Gly Thr Ser Leu Thr Phe His Ile Ile Phe Ala
435 440 445

Leu Leu Asn Ala Phe Gln Phe Phe Ile Leu Leu Phe Gly Thr Ile Met
450 455 460

Asp His Lys Val
465

<210> 20
<211> 1407
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic Organism

<400> 20
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tctgagaaca ttgtgaatga actcttcatt cagacaaaag ggtttcacat caaccataat 180

acctcagaga aaagcctcaa tttctccatg agcatgaaca ataccacaga agatatctta 240

ggaatggtac agattcccag gcaagagcta aggaagctgt ggccaaatgc atcccaagcc 300

attagcatag ctttcccaac cttgggggct atcctgagag aagcccactt gcaaaatgtg 360

agtcttccca gacaggtaaa tggtctggtg ctatcagtgg ttttaccaga aaggttgcaa 420

gaaatcatac tcaccttcga aaagatcaat aaaacccgca atgccagagc ccagtgtgtt 480

ggctggcact ccaagaaaag gagatgggat gagaaagcgt gccaaatgat gttggatatc 540

aggaacgaag tgaaatgccg ctgtaactac accagtgtgg tgatgtcttt ttccattctc 600

atgtcctcca aatcgatgac cgacaaagtt ctggactaca tcacctgcat tgggctcagc 660

gtctcaatcc taagcttggt tctttgcctg atcattgaag ccacagtgtg gtcccgggtg 720

gttgtgacgg agatatcata catgcgtcac gtgtgcatcg tgaatatagc agtgtccctt 780

ctgactgcca atgtgtggtt tatcataggc tctcacttta acattaaggc ccaggactac 840

aacatgtgtg ttgcagtgac atttttcagc cacttttttct acctctctct gtttttctgg 900

atgctcttca aagcattgct catcatttat ggaatattgg tcattttccg taggatgatg 960

aagtcccgaa tgatggtcat tggctttgcc attggctatg ggtgcccatt gatcattgct 1020

gtcactacag ttgctatcac agagccagag aaaggctaca taagacctga ggcctgttgg 1080

cttaactggg acaataccaa agccctttaa gcatttgcca tcccggcgtt cgtcattgtg 1140

gctgtaaatc tgattgtggt tttggttgtt gctgtcaaca ctcagaggcc ctctattggc 1200

agttccaagt ctcaggatgt ggtcataatt atgaggatca gcaaaaatgt tgccatcctc 1260

actccactgc tgggactgac ctggggtttt ggaatagcca ctctcataga aggcacttcc 1320

ttgacgttcc atataatttt tgccttgctc aatgctttcc agggtttttt catcctgctg 1380

tttggaacca ttatggatca caaggta 1407